SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> Homogentisat-Dioxygenase

<130> M/40226

<140> 19937957.2
<141> 1999-08-11

<160> 15

<170> PatentIn Ver. 2.1

<210> 1
<211> 575
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(6)
<223> /function= "Restriktionsschnittstelle

<220>
<221> misc_feature
<222> (570)..(575)
<223> /function = "Restriktionsschnittstelle"

<400> 1
gtcgacgggc cgatgggggc gaagggtctt gctgcaccaa gagattttct tgcaccaacg 60
gcatggtttg aggaagggct acggcctgac tacactattg ttcagaagtt tggcggtgaa 120
ctctttactg ctaaacaaga tttctctccg ttcaatgtgg ttgcctggca tggcaattac 180
gtgccttata agtatgacct gcacaagttc tgtccataca acactgtcct tgtagaccat 240
ggagatccat ctgtaaatac agttctgaca gcaccaacgg ataaacctgg tgtggccttg 300
cttgattttg tcatattccc tcctcgttgg ttggttgctg agcatacctt tcgacctcct 360
tactaccatc gtaactgcat gagtgaattt atgggcctaa tctatggtgc ttacgaggcc 420
aaagctgatg gatttctacc tggtggcgca agtcttcaca gttgtatgac acctcatggt 480
ccagatacaa ccacatacga ggcgacgatt gctcgtgtaa atgcaatggc tccttataag 540
ctcacaggca ccatggcctt catgtttgag gtacc 575

<210> 2
<211> 26
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz: /desc =
      "Oligonukleotid"

<220>
<221> misc_feature
<222> (9)
<223> /mod_base = i

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<220>
<221> misc_feature
<222> (12)
<223> /mod_base = i


<220>
<221> misc_feature
<222> (15)
<223> /mod_base = i


<220>
<221> misc_feature
<222> (18)
<223> /mod_base = i


<220>
<221> misc_feature
<222> (21)
<223> /mod_base = i


<220>
<221> misc_feature
<222> (24)
<223> /mod_base = i


<400> 2
gtcgacggnc cnatnggngc naangg                                    26



<210> 3
<211> 29
<212> DNA
<213> Künstliche Sequenz


<220>
<223> Beschreibung der künstlichen Sequenz: /desc =
      "Oligonukleotid"


<220>
<221> misc_feature
<222> (18)
<223> /mod_base = i


<220>
<221> misc_feature
<222> (24)
<223> /mod_base = i


<220>
<221> misc_feature
<222> (27)
<223> /mod_base = i


<400> 3
ggtacctcra acatraangc catngtncc                                 29
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<210> 4
<211> 25
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz: /desc =
      "Oligonukleotid"

<400> 4
gaattcgatc tgtcgtctca aactc                                        25


<210> 5
<211> 26
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz: /desc =
      "Oligonukleotid"

<400> 5
ggtaccgtga tagtaaacaa ctaatg                                       26


<210> 6
<211> 34
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz: /desc =
      "Oligonukleotid"

<400> 6
atggtacctt ttttgcataa acttatcttc atag                              34


<210> 7
<211> 43
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz: /desc =
      "Oligonukleotid"

<400> 7
atgtcgaccc gggatccagg gccctgatgg gtcccatttt ccc                    43


<210> 8
<211> 25
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<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz: /desc =
      Oligonukleotid"

<400> 8
gtcgacgaat ttccccgaat cgttc   25

<210> 9
<211> 24
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz: /desc =
      "Oligonukleotid"

<400> 9
aagcttccga tctagtaaca taga   24

<210> 10
<211> 25
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz: /desc =
      "Oligonukleotid"

<400> 10
aagcttgatc tgtcgtctca aactc   25

<210> 11
<211> 24
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz: /desc =
      "Oligonukleotid"

<400> 11
aagcttccga tctagtaaca taga   24

<210> 12
<211> 32
<212> DNA
<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz: /desc =
      "Oligonukleotid"

<400> 12
attctagaca tggagtcaaa gattcaaata ga   32

<210> 13
<211> 32
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz: /desc =
      "Oligonukleotid"

<400> 13
attctagagg acaatcagta aattgaacgg ag   32

<210> 14
<211> 1159
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz: /desc =
      "DNA"

<220>
<221> misc_feature
<222> (1)..(6)
<223> /function = "Restriktionsschnittstelle"

<220>
<221> CDS
<222> (8)..(1153)

<220>
<221> misc_feature
<222> (1154)..(1159)
<223> /function = "Restriktionsschnittstelle"

<400> 14
gtcgact atg act caa act act cat cat act cca gat act gct aga caa   49
        Met Thr Gln Thr Thr His His Thr Pro Asp Thr Ala Arg Gln
          1   5   10

gct gat cct ttt cca gtt aag gga atg gat gct gtt gtt ttc gct gtt   97
Ala Asp Pro Phe Pro Val Lys Gly Met Asp Ala Val Val Phe Ala Val
 15   20   25   30

gga aac gct aag caa gct gct cat tac tac tct act gct ttc gga atg   145
Gly Asn Ala Lys Gln Ala Ala His Tyr Tyr Ser Thr Ala Phe Gly Met
                 35   40   45

```
caa ctt gtt gct tac tct gga cca gaa aac gga tct aga gaa act gct    193
Gln Leu Val Ala Tyr Ser Gly Pro Glu Asn Gly Ser Arg Glu Thr Ala
            50                  55                  60

tct tac gtt ctt act aac gga tct gct aga ttc gtt ctt act tct gtt    241
Ser Tyr Val Leu Thr Asn Gly Ser Ala Arg Phe Val Leu Thr Ser Val
            65                  70                  75

att aag cca gct acc cca tgg gga cat ttc ctt gct gat cac gtt gct    289
Ile Lys Pro Ala Thr Pro Trp Gly His Phe Leu Ala Asp His Val Ala
            80                  85                  90

gaa cac gga gat gga gtt gtt gat ctt gct att gaa gtt cca gat gct    337
Glu His Gly Asp Gly Val Val Asp Leu Ala Ile Glu Val Pro Asp Ala
95                  100                 105                 110

aga gct gct cat gct tac gct att gaa cat gga gct aga tct gtt gct    385
Arg Ala Ala His Ala Tyr Ala Ile Glu His Gly Ala Arg Ser Val Ala
                115                 120                 125

gaa cca tac gaa ctt aag gat gaa cat gga act gtt gtt ctt gct gct    433
Glu Pro Tyr Glu Leu Lys Asp Glu His Gly Thr Val Val Leu Ala Ala
            130                 135                 140

att gct act tac gga aag act aga cat act ctt gtt gat aga act gga    481
Ile Ala Thr Tyr Gly Lys Thr Arg His Thr Leu Val Asp Arg Thr Gly
            145                 150                 155

tac gat gga cca tac ctt cca gga tac gtt gct gct gct cca att gtt    529
Tyr Asp Gly Pro Tyr Leu Pro Gly Tyr Val Ala Ala Ala Pro Ile Val
            160                 165                 170

gaa cca cca gct cat aga acc ttc caa gct att gac cat tgt gtt ggt    577
Glu Pro Pro Ala His Arg Thr Phe Gln Ala Ile Asp His Cys Val Gly
175                 180                 185                 190

aac gtt gaa ctc gga aga atg aac gaa tgg gtt gga ttc tac aac aag    625
Asn Val Glu Leu Gly Arg Met Asn Glu Trp Val Gly Phe Tyr Asn Lys
            195                 200                 205

gtt atg gga ttc act aac atg aag gaa ttc gtt gga gat gat att gct    673
Val Met Gly Phe Thr Asn Met Lys Glu Phe Val Gly Asp Asp Ile Ala
            210                 215                 220

act gag tac tct gct ctt atg tct aag gtt gtt gct gat gga act ctt    721
Thr Glu Tyr Ser Ala Leu Met Ser Lys Val Val Ala Asp Gly Thr Leu
            225                 230                 235

aag gtt aaa ttc cca att aat gaa cca gct ctt gct aag aag aag tct    769
Lys Val Lys Phe Pro Ile Asn Glu Pro Ala Leu Ala Lys Lys Lys Ser
            240                 245                 250

cag att gat gaa tac ctt gag ttc tac gga gga gct gga gtt caa cat    817
Gln Ile Asp Glu Tyr Leu Glu Phe Tyr Gly Gly Ala Gly Val Gln His
255                 260                 265                 270
```

```
att gct ctt aac act gga gat atc gtg gaa act gtt aga act atg aga        865
Ile Ala Leu Asn Thr Gly Asp Ile Val Glu Thr Val Arg Thr Met Arg
            275             280             285

gct gca gga gtt caa ttc ctt gat act cca gat tct tac tac gat act        913
Ala Ala Gly Val Gln Phe Leu Asp Thr Pro Asp Ser Tyr Tyr Asp Thr
            290             295             300

ctt ggt gaa tgg gtt gga gat act aga gtt cca gtt gat act ctt aga        961
Leu Gly Glu Trp Val Gly Asp Thr Arg Val Pro Val Asp Thr Leu Arg
            305             310             315

gaa ctt aag att ctt gct gat aga gat gaa gat gga tac ctt ctt caa       1009
Glu Leu Lys Ile Leu Ala Asp Arg Asp Glu Asp Gly Tyr Leu Leu Gln
            320             325             330

atc ttc act aag cca gtt caa gat aga cca act gtg ttc ttc gaa atc       1057
Ile Phe Thr Lys Pro Val Gln Asp Arg Pro Thr Val Phe Phe Glu Ile
335             340             345             350

att gaa aga cat gga tct atg gga ttc gga aag ggt aac ttc aag gct       1105
Ile Glu Arg His Gly Ser Met Gly Phe Gly Lys Gly Asn Phe Lys Ala
            355             360             365

ctt ttc gaa gct att gaa aga gaa caa gag aag aga gga aac ctt tag       1153
Leu Phe Glu Ala Ile Glu Arg Glu Gln Glu Lys Arg Gly Asn Leu
            370             375             380

gtcgac                                                                 1159
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<210> 15
<211> 381
<212> PRT
<213> Künstliche Sequenz
<223> Beschreibung der künstlichen Sequenz: /desc =
      "DNA"

<400> 15
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Met Thr Gln Thr Thr His His Thr Pro Asp Thr Ala Arg Gln Ala Asp
 1               5               10              15

Pro Phe Pro Val Lys Gly Met Asp Ala Val Val Phe Ala Val Gly Asn
            20              25              30

Ala Lys Gln Ala Ala His Tyr Tyr Ser Thr Ala Phe Gly Met Gln Leu
            35              40              45

Val Ala Tyr Ser Gly Pro Glu Asn Gly Ser Arg Glu Thr Ala Ser Tyr
            50              55              60

Val Leu Thr Asn Gly Ser Ala Arg Phe Val Leu Thr Ser Val Ile Lys
65              70              75              80

Pro Ala Thr Pro Trp Gly His Phe Leu Ala Asp His Val Ala Glu His
                85              90              95
```

```
Gly Asp Gly Val Val Asp Leu Ala Ile Glu Val Pro Asp Ala Arg Ala
        100                     105             110

Ala His Ala Tyr Ala Ile Glu His Gly Ala Arg Ser Val Ala Glu Pro
        115                 120                 125

Tyr Glu Leu Lys Asp Glu His Gly Thr Val Val Leu Ala Ala Ile Ala
    130                 135                 140

Thr Tyr Gly Lys Thr Arg His Thr Leu Val Asp Arg Thr Gly Tyr Asp
145                 150                 155                 160

Gly Pro Tyr Leu Pro Gly Tyr Val Ala Ala Ala Pro Ile Val Glu Pro
            165                 170                 175

Pro Ala His Arg Thr Phe Gln Ala Ile Asp His Cys Val Gly Asn Val
            180                 185                 190

Glu Leu Gly Arg Met Asn Glu Trp Val Gly Phe Tyr Asn Lys Val Met
        195                 200                 205

Gly Phe Thr Asn Met Lys Glu Phe Val Gly Asp Asp Ile Ala Thr Glu
    210                 215                 220

Tyr Ser Ala Leu Met Ser Lys Val Val Ala Asp Gly Thr Leu Lys Val
225                 230                 235                 240

Lys Phe Pro Ile Asn Glu Pro Ala Leu Ala Lys Lys Lys Ser Gln Ile
            245                 250                 255

Asp Glu Tyr Leu Glu Phe Tyr Gly Gly Ala Gly Val Gln His Ile Ala
            260                 265                 270

Leu Asn Thr Gly Asp Ile Val Glu Thr Val Arg Thr Met Arg Ala Ala
        275                 280                 285

Gly Val Gln Phe Leu Asp Thr Pro Asp Ser Tyr Tyr Asp Thr Leu Gly
    290                 295                 300

Glu Trp Val Gly Asp Thr Arg Val Pro Val Asp Thr Leu Arg Glu Leu
305                 310                 315                 320

Lys Ile Leu Ala Asp Arg Asp Glu Asp Gly Tyr Leu Leu Gln Ile Phe
            325                 330                 335

Thr Lys Pro Val Gln Asp Arg Pro Thr Val Phe Phe Glu Ile Ile Glu
            340                 345                 350

Arg His Gly Ser Met Gly Phe Gly Lys Gly Asn Phe Lys Ala Leu Phe
        355                 360                 365

Glu Ala Ile Glu Arg Glu Gln Glu Lys Arg Gly Asn Leu
    370                 375                 380
```